



TSUNEOKA Seq. Listing revised and filed 2006-02-03

Sequence Listing

<110> TSUNEOKA, Makoto
KIMURA, Hiroshi

<120> Cancer-Associated Gene Mina53, Protein Mina53
and Monoclonal Antibody Thereof

<130> 2004-1597A/WMC/00279

<140> 10/509,073

<141> 2005-01-12

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<211> 1395

<212> DNA

<213> Homo sapiens

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Ala Pro Cys Lys Gln Met Lys leu Glu Ala Ala Gly Gly Pro Ser Ala	
20 25 30	
tta aac ttt gac agt ccc agt agt ctc ttt gaa agt tta atc tcg ccc	144
Leu Asn Phe Asp Ser Pro Ser Ser Leu Phe Glu Ser Leu Ile Ser Pro	
35 40 45	
atc aag aca gag act ttt ttc aag gaa ttc tgg gag cag aag ccc ctt	192
Ile Lys Thr Glu Thr Phe Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu	
50 55 60	
ctc att cag aga gat gac cct gca ctg gcc aca tac tat ggg tcc ctg	240
Leu Ile Gln Arg Asp Asp Pro Ala Leu Ala Thr Tyr Tyr Gly Ser Leu	
65 70 75 80	
ttc aag cta aca gat ctg aag agt ctg tgc agc cgg ggg atg tac tat	288
Phe Lys Leu Thr Asp Leu Lys Ser Leu Cys Ser Arg Gly Met Tyr Tyr	
85 90 95	
gga aga gat gtg aat gtc tgc cgg tgt gtc aat ggg aag aag aag gtt	336
Gly Arg Asp Val Asn Val Cys Arg Cys Val Asn Gly Lys Lys Lys Val	
100 105 110	
tta aat aaa gat ggc aaa gca cac ttt ctt cag ctg aga aaa gat ttt	384
Leu Asn Lys Asp Gly Lys Ala His Phe Leu Gln Leu Arg Lys Asp Phe	
115 120 125	
gat cag aaa agg gca acg att cag ttt cac caa cct cag aga ttt aag	432
Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Phe Lys	
130 135 140	
gat gag ctt tgg agg atc cag gag aag ctg gaa tgt tac ttt ggc tcc	480
Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser	
145 150 155 160	
ttg gtt ggc tcg aat gtg tac ata act ccc gca gga tct cag ggc ctg	528

TSUNEOKA Seq. Listing revised and filed 2006-02-03

Leu	Val	Gly	Ser	Asn	Val	Tyr	Ile	Thr	Pro	Ala	Gly	Ser	Gln	Gly	Leu	
				165					170					175		
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gag	aaa	cac	tgg	cg	ctc	tac	cac	ccc	act	gtg	ccc	ctg	gca	cga	gag	624
Glu	Lys	His	Trp	Arg	Leu	Tyr	His	Pro	Thr	Val	Pro	Leu	Ala	Arg	Glu	
		195					200					205				
tac	agc	gtg	gag	gcc	gag	gaa	agg	atc	ggc	agg	ccg	gtg	cat	gag	ttt	672
Tyr	Ser	Val	Glu	Ala	Glu	Glu	Arg	Ile	Gly	Arg	Pro	Val	His	Glu	Phe	
	210					215					220					
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Ser	Thr	Tyr	Gln	Asn	Asn	Ser	Trp	Gly	Asp	Phe	Leu	Leu	Asp	Thr	Ile	
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Ser	Gly	Leu	Val	Phe	Asp	Thr	Ala	Lys	Glu	Asp	Val	Glu	Leu	Arg	Thr	
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Arg	Leu	Pro	Pro	Tyr	Ser	Ala	Gly	Asp	Gly	Ala	Glu	Leu	Ser	Thr	Pro	
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Asp	His	Ile	Val	Leu	Thr	Val	Leu	Pro	Asp	Gln	Asp	Gln	Ser	Asp	Glu	
	370					375					380					
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	385				390					395					400	
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TSUNEOKA Seq. Listing revised and filed 2006-02-03

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cca gct att tct gtc aag gac ctg aaa ctt act aca gat gag gaa aag	1344
Pro Ala Ile Ser Val Lys Asp Leu Lys Leu Thr Thr Asp Glu Glu Lys	
435 440 445	
gaa agc ctg gta tta tcc ctc tgg aca gaa tgt tta att caa gta gtc	1392
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gtt cct tgc aag cgg gtg aag gag gag ctg cct gaa acg ctt tct gta	96
Val Pro Cys Lys Arg Val Lys Glu Glu Leu Pro Glu Thr Leu Ser Val	
20 25 30	
tta aac ttt gac agc ccc agt agt ttc ttc gaa agt tta atc tca ccc	144
Leu Asn Phe Asp Ser Pro Ser Ser Phe Phe Glu Ser Leu Ile Ser Pro	
35 40 45	
atc aaa gta gag act ttt ttc aag gaa ttc tgg gaa caa aag ccc ctt	192
Ile Lys Val Glu Thr Phe Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu	
50 55 60	
ctc att cag agg gat gac cct gta ctg gcc aaa tat tac cag tct ctg	240
Leu Ile Gln Arg Asp Asp Pro Val Leu Ala Lys Tyr Tyr Gln Ser Leu	
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ttc agc ctc tca gat ctg aag aga ctc tgc aag aaa gga gtg tac tat	288
Phe Ser Leu Ser Asp Leu Lys Arg Leu Cys Lys Lys Gly Val Tyr Tyr	
85 90 95	
gga aga gac gtg aat gtc tgc cgg agc atc agt ggg aag aag aag gtt	336
Gly Arg Asp Val Asn Val Cys Arg Ser Ile Ser Gly Lys Lys Lys Val	
100 105 110	
tta aat aag gat ggc aga gca cat ttt ctt cag ctg aga aaa gat ttt	384
Leu Asn Lys Asp Gly Arg Ala His Phe Leu Gln Leu Arg Lys Asp Phe	
115 120 125	
gat cag aag agg gca aca att cag ttt cac caa cct cag aga tat aag	432
Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Tyr Lys	
130 135 140	
gat gag ctg tgg cgg atc cag gaa aag ctg gaa tgt tac ttt ggg tcc	480
Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser	
145 150 155 160	

TSUNEOKA Seq. Listing revised and filed 2006-02-03

tta gta ggc tct aat gtg tac atg act cct gca gga tct cag ggc ctc	528
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cct cca cat tat gat gat gtt gag gtt ttt atc ctg cag ctg gag gga	576
Pro Pro His Tyr Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly	
180 185 190	
acg aaa cac tgg cgc ctg tac tcc cca act gtg ccc ctg gca cac gag	624
Thr Lys His Trp Arg Leu Tyr Ser Pro Thr Val Pro Leu Ala His Glu	
195 200 205	
tac agt gtg gaa tct gag gac cgg atc ggc aca ccg aca cac gac ttc	672
Tyr Ser Val Glu Ser Glu Asp Arg Ile Gly Thr Pro Thr His Asp Phe	
210 215 220	
ctg ctg aag cct gga gat ttg ttg tac ttt ccc aga ggg acc att cat	720
Leu Leu Lys Pro Gly Asp Leu Leu Tyr Phe Pro Arg Gly Thr Ile His	
225 230 235 240	
cag gca gaa act cct tca ggc ctg gcc tac tct att cac ctg act att	768
Gln Ala Glu Thr Pro Ser Gly Leu Ala Tyr Ser Ile His Leu Thr Ile	
245 250 255	
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Ser Thr Tyr Gln Asn Asn Ser Trp Gly Asp Cys Leu Leu Asp Ser Ile	
260 265 270	
tcg ggg ttc gta ttt gac att gca aag gaa gat gtg gca tta agg agt	864
Ser Gly Phe Val Phe Asp Ile Ala Lys Glu Asp Val Ala Leu Arg Ser	
275 280 285	
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290 295 300	
aca agg aag ttg agt ggc ttt ctg agg act ctt gca gac cag ctc gag	960
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305 310 315 320	
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His Arg Leu Pro Pro Phe Phe Glu Gly Asn Gly Thr Glu Thr Met Asp	
340 345 350	
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Pro Gly Lys Gln Leu Pro Arg Leu Asp Asn Ile Ile Arg Leu Gln Phe	
355 360 365	
aaa gat cac att gtc ctc aca gta ggg cca gat aag aat cca ttt gat	1152
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370 375 380	
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385 390 395 400	
agg cag atg cac atg ata gga gaa gag gag gaa tcc gag att ttc ggt	1248
Arg Gln Met His Met Ile Gly Glu Glu Glu Glu Ser Glu Ile Phe Gly	

TSUNEOKA Seq. Listing revised and filed 2006-02-03
405 410 415

ctt cgc ttt cct tta tca cat gtg gat gct ctg aag caa atc tgg tgc 1296
Leu Arg Phe Pro Leu Ser His Val Asp Ala Leu Lys Gln Ile Trp Cys
420 425 430

ggg tca cca att cgt gtt aag gaa ctg aaa ctt gac aca gat gaa gaa 1344
Gly Ser Pro Ile Arg Val Lys Glu Leu Lys Leu Asp Thr Asp Glu Glu
435 440 445

aag gag aac ctg gca ctg tct ctc tgg tcg gag tct tta atc caa gta 1392
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Leu
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Val Pro Cys Lys Gln Val Lys Glu Glu Leu Pro Asn Thr Leu Ser Val
20 25 30

tta aac ttt gac agc ccc agt agt ttc ttt gaa agt tta ata tca ccc 144
Leu Asn Phe Asp Ser Pro Ser Ser Phe Phe Glu Ser Leu Ile Ser Pro
35 40 45

atc aaa gta gag aca ttt ttc aag gaa ttc tgg gaa cag aag ccc ctt 192
Ile Lys Val Glu Thr Phe Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu
50 55 60

ctc att cag aga gat gac cct tcg ctg gcc gca tat tac cag tct ctg 240
Leu Ile Gln Arg Asp Asp Pro Ser Leu Ala Ala Tyr Tyr Gln Ser Leu
65 70 75 80

ttc agc ctc tca gat ctg agg agt ctc tgc agc caa ggg ctg tac tat 288
Phe Ser Leu Ser Asp Leu Arg Ser Leu Cys Ser Gln Gly Leu Tyr Tyr
85 90 95

gga aga gat gtc aat gtc tgc cgg tgc atc ggt ggg aag aag aag gtt 336
Gly Arg Asp Val Asn Val Cys Arg Cys Ile Gly Gly Lys Lys Lys Val
100 105 110

tta aat aag gat ggc aaa gca cag ttt ctt cag ctg aga aaa gat ttt 384
Leu Asn Lys Asp Gly Lys Ala Gln Phe Leu Gln Leu Arg Lys Asp Phe
115 120 125

gat cag aag agg gca aca att cag ttt cat cag cca cag aga ttt aag 432
Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Phe Lys
130 135 140

gat gag ctc tgg agg atc cag gaa aag ctg gaa tgt tac ttt ggc tcc 480
Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser
Page 5

TSUNEOKA Seq. Listing revised and filed 2006-02-03

145		150		155		160	
tta gta ggc tca aat gtg tac atg act ccc gca gga tct cag ggc ctt	528						
Leu Val Gly Ser Asn Val Tyr Met Thr Pro Ala Gly Ser Gln Gly Leu							
		165		170		175	
cct cca cat tac gac gat gtt gag gtt ttt atc ctg cag ctg gag gga	576						
Pro Pro His Tyr Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly							
		180		185		190	
agg aaa cgt tgg cgc ctg tac tcc cca act gtg ccc ctg gcg cgt gag	624						
Arg Lys Arg Trp Arg Leu Tyr Ser Pro Thr Val Pro Leu Ala Arg Glu							
		195		200		205	
tac agt gtg gag cct gag gac cgg att ggc aca cca aca cat gac ttc	672						
Tyr Ser Val Glu Pro Glu Asp Arg Ile Gly Thr Pro Thr His Asp Phe							
		210		215		220	
ctg ctg aag cct ggc gat ttg ttg tac ttc ccc aga ggg acc att cac	720						
Leu Leu Lys Pro Gly Asp Leu Leu Tyr Phe Pro Arg Gly Thr Ile His							
		225		230		235	
cag gca gaa act cct tca ggc ctg gcc cac tct att cac ctg act att	768						
Gln Ala Glu Thr Pro Ser Gly Leu Ala His Ser Ile His Leu Thr Ile							
		245		250		255	
agc acc tac cag aac aat tca tgg gga gat tac ctt ttg gac tcc att	816						
Ser Thr Tyr Gln Asn Asn Ser Trp Gly Asp Tyr Leu Leu Asp Ser Ile							
		260		265		270	
tcg ggg ctt gta ttt gac att gca aag gaa gat gtg gca tta agg act	864						
Ser Gly Leu Val Phe Asp Ile Ala Lys Glu Asp Val Ala Leu Arg Thr							
		275		280		285	
gga atg ccc agg cgg atg ctc atg aat gtg gaa acc cca gct gac gta	912						
Gly Met Pro Arg Arg Met Leu Met Asn Val Glu Thr Pro Ala Asp Val							
		290		295		300	
aca agg aag ttg agt ggc ttt ctg agg act ctg gca gac cag ctc gag	960						
Thr Arg Lys Leu Ser Gly Phe Leu Arg Thr Leu Ala Asp Gln Leu Glu							
		305		310		315	
ggc aga aaa gaa ctg ctc tca tca gat atg aag aag gac ttc gtc atg	1008						
Gly Arg Lys Glu Leu Ser Ser Asp Met Lys Lys Asp Phe Val Met							
		325		330		335	
cac aga ctt ccc cct ttc tgt gtg gga aat gga aca gag tca atg aac	1056						
His Arg Leu Pro Pro Phe Cys Val Gly Asn Gly Thr Glu Ser Met Asn							
		340		345		350	
cca ggt gga aag ttg cca agg ttg aac agc ata gta aga ctg cag ttt	1104						
Pro Gly Gly Lys Leu Pro Arg Leu Asn Ser Ile Val Arg Leu Gln Phe							
		355		360		365	
aaa gac cac att gtc ctc aca gta ggg ccc gat cag aat caa tct gat	1152						
Lys Asp His Ile Val Leu Thr Val Gly Pro Asp Gln Asn Gln Ser Asp							
		370		375		380	
gaa gct caa caa aag gtg gtt tac atc tac cat tct cta aag aat gag	1200						
Glu Ala Gln Gln Lys Val Val Tyr Ile Tyr His Ser Leu Lys Asn Glu							
		385		390		395	
aga cag acg cac atg atg ggg aaa gag gtg gaa aca gag att tat gga	1248						

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Arg	Gln	Thr	His	Met	Met	Gly	Lys	Glu	Val	Glu	Thr	Glu	Ile	Tyr	Gly		
				405					410					415			
ctt	cgc	ttt	cct	tta	tcc	tat	gtg	gac	gct	ctg	aag	caa	atc	tgg	tgc	1296	
Leu	Arg	Phe	Pro	Leu	Ser	Tyr	Val	Asp	Ala	Leu	Lys	Gln	Ile	Trp	Cys		
			420					425					430				
ggg	tca	cca	gtt	cgt	gtt	aag	gac	ctg	aaa	ctt	ggc	aca	gat	gaa	gag	1344	
Gly	Ser	Pro	Val	Arg	Val	Lys	Asp	Leu	Lys	Leu	Gly	Thr	Asp	Glu	Glu		
		435					440					445					
aag	gag	aac	ctg	gca	gtg	tct	ctc	tgg	aca	gag	tgt	cta	gtc	cac	gtg	1392	
Lys	Glu	Asn	Leu	Ala	Val	Ser	Leu	Trp	Thr	Glu	Cys	Leu	Val	His	Val		
	450					455					460						
ctc	tag															1398	
Leu																	
465																	